

SEQUENCE LISTING

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(1) GENERAL INFORMATION

(i) APPLICANT: Jaspers, Stephen R.
Sprugel, Katherine H.
Ren, Hong Ping
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Conklin, Darrell C.

(ii) TITLE OF THE INVENTION: COMPOSITIONS AND METHODS FOR
STIMULATING PANCREATIC ISLET CELL REGENERATION

(iii) NUMBER OF SEQUENCES: 7

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: ZymoGenetics, Inc.
(B) STREET: 1201 Eastlake Avenue East
(C) CITY: Seattle
(D) STATE: WA
(E) COUNTRY: USA
(F) ZIP: 98102

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 60/033,003
(B) FILING DATE: December 16, 1996

(viii) ATTORNEY/AGENT INFORMATION:

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(C) REFERENCE/DOCKET NUMBER: 96-41

(ix) TELECOMMUNICATION INFORMATION:

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(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 420 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...417

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG GCC AGC CTG TTC CGG TCC TAT CTG CCA GCA ATC TGG CTG CTG CTG 48
Met Ala Ser Leu Phe Arg Ser Tyr Leu Pro Ala Ile Trp Leu Leu Leu
1 5 10 15

AGC CAA CTC CTT AGA GAA AGC CTA GCA GCA GAG CTG AGG GGA TGT GGT 96
Ser Gln Leu Leu Arg Glu Ser Leu Ala Ala Glu Leu Arg Gly Cys Gly
20 25 30

CCC CGA TTT GGA AAA CAC TTG CTG TCA TAT TGC CCC ATG CCT GAG AAG 144
Pro Arg Phe Gly Lys His Leu Leu Ser Tyr Cys Pro Met Pro Glu Lys
35 40 45

ACA TTC ACC ACC ACC CCA GGA GGG TGG CTG CTG GAA TCT GGA CGT CCC 192
Thr Phe Thr Thr Thr Pro Gly Gly Trp Leu Leu Glu Ser Gly Arg Pro
50 55 60

AAA GAA ATG GTG TCA ACC TCC AAC AAC AAA GAT GGA CAA GCC TTA GGT 240
Lys Glu Met Val Ser Thr Ser Asn Asn Lys Asp Gly Gln Ala Leu Gly
65 70 75 80

ACG ACA TCA GAA TTC ATT CCT AAT TTG TCA CCA GAG CTG AAG AAA CCA	288
Thr Thr Ser Glu Phe Ile Pro Asn Leu Ser Pro Glu Leu Lys Lys Pro	
85 90 95	
CTG TCT GAA GGG CAG CCA TCA TTG AAG AAA ATA ATA CTT TCC CGC AAA	336
Leu Ser Glu Gly Gln Pro Ser Leu Lys Lys Ile Ile Leu Ser Arg Lys	
100 105 110	
AAG AGA AGT GGA CGT CAC AGA TTT GAT CCA TTC TGT TGT GAA GTA ATT	384
Lys Arg Ser Gly Arg His Arg Phe Asp Pro Phe Cys Cys Glu Val Ile	
115 120 125	
TGT GAC GAT GGA ACT TCA GTT AAA TTA TGT ACA TAG	420
Cys Asp Asp Gly Thr Ser Val Lys Leu Cys Thr	
130 135	

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Ala	Ser	Leu	Phe	Arg	Ser	Tyr	Leu	Pro	Ala	Ile	Trp	Leu	Leu	Leu
1			5					10					15		
Ser	Gln	Leu	Leu	Arg	Glu	Ser	Leu	Ala	Ala	Glu	Leu	Arg	Gly	Cys	Gly
	20						25						30		
Pro	Arg	Phe	Gly	Lys	His	Leu	Leu	Ser	Tyr	Cys	Pro	Met	Pro	Glu	Lys
	35					40					45				
Thr	Phe	Thr	Thr	Thr	Pro	Gly	Gly	Trp	Leu	Leu	Glu	Ser	Gly	Arg	Pro
	50					55				60					
Lys	Glu	Met	Val	Ser	Thr	Ser	Asn	Asn	Lys	Asp	Gly	Gln	Ala	Leu	Gly
65				70					75					80	
Thr	Thr	Ser	Glu	Phe	Ile	Pro	Asn	Leu	Ser	Pro	Glu	Leu	Lys	Lys	Pro
			85					90					95		
Leu	Ser	Glu	Gly	Gln	Pro	Ser	Leu	Lys	Lys	Ile	Ile	Leu	Ser	Arg	Lys
		100					105					110			

Lys Arg Ser Gly Arg His Arg Phe Asp Pro Phe Cys Cys Glu Val Ile
 115 120 125
 Cys Asp Asp Gly Thr Ser Val Lys Leu Cys Thr
 130 135

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 480 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...477
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATG GAT GCA ATG AAG AGA GGG CTC TGC TGT GTG CTG CTG CTG TGT GGC	48
Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly	
1 5 10 15	
GCC GTC TTC GTT TCG CCC AGC CAG GAA ATC CAT GCC GAG TTC CAG AGA	96
Ala Val Phe Val Ser Pro Ser Gln Glu Ile His Ala Glu Phe Gln Arg	
20 25 30	
GGA CGC AGA CAT CAC CAT CAC CAT CAC GGT GGC TCC GGA GCA GAG CTG	144
Gly Arg Arg His His His His His His Gly Gly Ser Gly Ala Glu Leu	
35 40 45	
AGG GGA TGT GGT CCC CGA TTT GGA AAA CAC TTG CTG TCA TAT TGC CCC	192
Arg Gly Cys Gly Pro Arg Phe Gly Lys His Leu Leu Ser Tyr Cys Pro	
50 55 60	
ATG CCT GAG AAG ACA TTC ACC ACC ACC CCA GGA GGG TGG CTG CTG GAA	240
Met Pro Glu Lys Thr Phe Thr Thr Thr Pro Gly Gly Trp Leu Leu Glu	
65 70 75 80	
TCT GGA CGT CCC AAA GAA ATG GTG TCA ACC TCC AAC AAC AAA GAT GGA	288
Ser Gly Arg Pro Lys Glu Met Val Ser Thr Ser Asn Asn Lys Asp Gly	
85 90 95	

CAA GCC TTA GGT ACG ACA TCA GAA TTC ATT CCT AAT TTG TCA CCA GAG 336
 Gln Ala Leu Gly Thr Thr Ser Glu Phe Ile Pro Asn Leu Ser Pro Glu
 100 105 110

CTG AAG AAA CCA CTG TCT GAA GGG CAG CCA TCA TTG AAG AAA ATA ATA 384
 Leu Lys Lys Pro Leu Ser Glu Gly Gln Pro Ser Leu Lys Lys Ile Ile
 115 120 125

CTT TCC CGC AAA AAG AGA AGT GGA CGT CAC AGA TTT GAT CCA TTC TGT 432
 Leu Ser Arg Lys Lys Arg Ser Gly Arg His Arg Phe Asp Pro Phe Cys
 130 135 140

TGT GAA GTA ATT TGT GAC GAT GGA ACT TCA GTT AAA TTA TGT ACA TAG 480
 Cys Glu Val Ile Cys Asp Asp Gly Thr Ser Val Lys Leu Cys Thr
 145 150 155

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly
 1 5 10 15
 Ala Val Phe Val Ser Pro Ser Gln Glu Ile His Ala Glu Phe Gln Arg
 20 25 30
 Gly Arg Arg His His His His His His Gly Gly Ser Gly Ala Glu Leu
 35 40 45
 Arg Gly Cys Gly Pro Arg Phe Gly Lys His Leu Leu Ser Tyr Cys Pro
 50 55 60
 Met Pro Glu Lys Thr Phe Thr Thr Thr Pro Gly Gly Trp Leu Leu Glu
 65 70 75 80
 Ser Gly Arg Pro Lys Glu Met Val Ser Thr Ser Asn Asn Lys Asp Gly
 85 90 95
 Gln Ala Leu Gly Thr Thr Ser Glu Phe Ile Pro Asn Leu Ser Pro Glu
 100 105 110

Leu Lys Lys Pro Leu Ser Glu Gly Gln Pro Ser Leu Lys Lys Ile Ile
 115 120 125
 Leu Ser Arg Lys Lys Arg Ser Gly Arg His Arg Phe Asp Pro Phe Cys
 130 135 140
 Cys Glu Val Ile Cys Asp Asp Gly Thr Ser Val Lys Leu Cys Thr
 145 150 155

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Asp Tyr Lys Asp Asp Asp Asp Lys Gly Ser Ala Glu Leu Arg Gly Cys
 1 5 10 15
 Gly Pro Arg Phe Gly Lys His Leu Leu Ser Tyr Cys Pro Met Pro Glu
 20 25 30
 Lys Thr Phe Thr Thr Thr Pro Gly Gly Trp Leu Leu Glu Ser Gly Arg
 35 40 45
 Pro Lys Glu Met Val Ser Thr Ser Asn Asn Lys Asp Gly Gln Ala Leu
 50 55 60
 Gly Thr Thr Ser Glu Phe Ile Pro Asn Leu Ser Pro Glu Leu Lys Lys
 65 70 75 80
 Pro Leu Ser Glu Gly Gln Pro Ser Leu Lys Lys Ile Ile Leu Ser Arg
 85 90 95
 Lys Lys Arg Ser Gly Arg His Arg Phe Asp Pro Phe Cys Cys Glu Val
 100 105 110
 Ile Cys Asp Asp Gly Thr Ser Val Lys Leu Cys Thr
 115 120

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Leu Cys Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys
1 5 10

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
(B) LOCATION: 3...5
(D) OTHER INFORMATION: Xaa is any amino acid except Cys

- (A) NAME/KEY: Other
(B) LOCATION: 7...14
(D) OTHER INFORMATION: Xaa is any amino acid except Cys

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Cys Cys Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys
1 5 10 15